

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

DECLARATION OF DR. YITZHAK PILPEL UNDER 37 C.F.R. § 1.132

I, Yitzhak Pilpel (Ph.D.), hereby declare as follows:

1. I am currently employed as a faculty member at the Department of Molecular Genetics of the Weizmann Institute, Israel. A true and correct copy of my *Curriculum Vitae* is attached to this declaration as Exhibit A. I am an author of 33 peer-reviewed scientific publications, of which 3 are related to microRNAs ("miRNAs"). I have supervised at least five experiments relating to microRNAs including computational analyses of the mammalian microRNA and other non-coding regulatory RNA network, and experimental verification of the informatic predictions.
2. A nucleic acid sequence of length 18-25 (endogenous or synthetic), which is predicted by a microRNA target algorithm, to bind to the 3' UTR of a mRNA in a manner characteristic of miRNA:mRNA binding, when co-expressed with the target mRNA (such as in an in vitro reporter gene assay), is likely to inhibit expression of the protein encoded by that mRNA.
3. Binding of microRNA to mRNA is characterized by **a)** 5'-end 'seed' (full complementary between the first 1-8 base pairs of the 5' of a mir and its target), conserved, often flanked by adenosines; **b)** Compensatory 3'-end in cases in which there is insufficient base-pairing of the microRNA 5' seed; and **c)** Multiple binding sites on the same mRNA targets which are not obligatory but enhance the binding effect on target repression. The above characteristics were described by various publications, including: Lai and Starck (Nat Genet, 2002; PLoS Biol., 2003), Doench and Sharp (Genes Dev., 2004), Lai (Genome Biol., 2004), Vella et. al. (Chem. Biol., 2004) and Brennecke et. al. (PLoS Biol., 2005)
4. The effectiveness of microRNA targets prediction algorithms that are based on the above characteristics has been described by numerous studies. As an example, Lewis et. al. (Cell 2003), reported a microRNA target prediction algorithm, TargetScan, which is based on the above mentioned characteristics, and have biologically validated 11 out of 15 predicted targets tested, estimating the algorithm's false positive rate to be between 22 and 31 percent. Another algorithm, called miRanda (Enright et. al., Genome Biol. 2003), correctly recovered 9 out of 10 biologically validated targets, with an estimated 24-39% false positive rate.
5. **Table A** below provides a list of characteristic nucleic-acid-sequences:mRNA bindings, taken from Rosetta Genomics patent applications. These nucleic acid sequences exhibit the characteristics of miRNA:mRNA bindings described above, and therefore are likely to inhibit their respective targets where co-expressed (such as in an in vitro reporter gene assay). Indeed, nearly all of the listed bindings are similarly detected by the above mentioned TargetScan algorithm, and half of them are further either detected by the miRanda algorithm, and/or are evolutionarily conserved.

6. It is my opinion that each sequence in column A would likely inhibit the expression of a protein encoded by the target gene in column B in view of the characteristics of miRNA:mRNA binding described above in paragraph 3.
7. I declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of any patent application relying on this declaration or any patent issuing thereon.

Dated March 19 -- By Roche Pilpel
2008

<p>Nucleic acid seqID:GAM_701317/53410</p>	<p>human neuronal tumor. Another location of GAX131410 is in another MAPKAPK2, a GAX131410 human target gene, which encodes for a protein kinase that mediates intracellular response to extracellular stimuli. It is also important for RNA splicing. MAPKAPK2 is associated with breast cancer disease, and therefore GAX131410 is associated with the developmental disease. Accordingly, the utilities of GAX131410 include the diagnosis, prevention and treatment of breast cancer and of other diseases and clinical conditions associated with MAPKAPK2. The function of MAPKAPK2 and its association with various diseases and clinical conditions has been established by previous studies, as described hereinafter with reference to GAX131410.</p>
<p>***** Filed in US patent application no.10/710,577</p>	<p>Target gene</p> <p>5' --- C---3' 3' AAGATGG TGTGG 5'</p> <p>Nucleic-acid</p> <p>13/22 complementary base pairs</p> <p>Table 7_A (Lines 50804-50898) Target/seqID: SET/5661481 Nucleic acid seqID:GAM_701403/53410</p> <p>***SET gene (SET, Accession number: NM_003613) is another GAX131410 target gene that is encoded by the human genome. SET (B10396) SET1 through SET18 (B10397-SET18) are human target binding sites that are found in the untranslated regions of mRNA encoded by the SET gene, corresponding to target binding sites such as SET1 (B10396) SET11 (B10397) or SET18 (B10398). Additionally, using the binding site prediction system of the present invention, GAX131410 binds to sequences on nucleosome 117R of mouse (NM_023871). The nucleotide sequences of SET (B10396) SET1 through SET18 (B10397-SET18) and the complementarity secondary structure to the nucleotide sequence of GAX131410 RNA are set forth in Tables 6-7, hereby incorporated herein. Another location of GAX131410 is in another SET, a GAX131410 human target gene which may be involved in intracellular signaling that regulates transcriptional activity. It may be involved in the inhibition of phosphatase 2A. SET is associated with leukemia disease, and therefore GAX131410 is associated with the developmental disease. Accordingly, the utilities of GAX131410 include the diagnosis, prevention and treatment of leukemia and of other diseases and clinical conditions associated with SET. The function of SET and its association with various diseases and clinical conditions has been established by previous studies, as described hereinafter with reference to GAX131410.</p>

1. These sequences are not depicted in Figure 13.1 data sheet.
 2. Target/seqID: (lines 50804-50898)
 3. Target/seqID: (lines 50804-50898)
 4. Target/seqID: (lines 50804-50898)

Curriculum Vitae

Yitzhak Pilpel

A: Personal Details

Date of birth: 12/9/1968
Place of birth: Jerusalem, Israel
Marital status: Married + 3 children
Military service: Four years' service in the IDF
Citizenship: Israeli
Mailing Address:
Dept. of Molecular Genetics
Weizmann Institute of Science
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Lab home page: <http://longitude.weizmann.ac.il>

B: Education

- 2000 - 2002 Postdoctoral Fellow. Department of Genetics, Harvard Medical School, Boston, MA, USA. Advisor: Prof. George M. Church.
- 1995 - 1999 Ph.D. degree. Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, Israel. Thesis title: Structural and evolutionary genomics of molecular recognition repertoires. Advisors: Prof. Doron Lancet; Prof. Ephraim Katchalski-Katzir.
- 1994 - 1995 Studies toward M.Sc. degree; transfer to direct Ph.D. track. Department of Membrane Research and Biophysics, Weizmann Institute of Science, Rehovot, Israel. Advisors: Prof. Doron Lancet; Prof. Ephraim Katchalski-Katzir.
- 1990 - 1993 B.Sc. degree. Major: Biology. Tel-Aviv University, Tel-Aviv, Israel.

C: Employment History

- 2003 - present Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, Israel. Senior Scientist, group leader.
Incumbent of the Aser Rothstein Career Development Chair of Genetic Diseases.

D: Academic Administration

- 2004 - present Feinberg Graduate School, Weizmann Institute of Science, Rehovot, Israel. Head of the Graduate Program in Bioinformatics.

E. Other Appointments

• Positions in academia and membership on committees

- 2007 - present Feinberg Graduate School, Weizmann Institute of Science, Rehovot, Israel. Member of the Board of Studies, Life Sciences.
- 2003-present Head Bioinformatics graduate program at the Feinberg Graduate School, Weizmann Institute of Science, Rehovot, Israel.

• Teaching experience - courses taught

- 2003-2006 Developed and taught the course, "Computational Functional Genomics." Feinberg Graduate School, Weizmann Institute of Science.
- 1998 Teaching Assistant for the course, "Programming for Bioinformatics and Internet." Feinberg Graduate School, Weizmann Institute of Science.
- 1997 Lecturer for the course, "Computational Genomic and Bioinformatics." Feinberg Graduate School, Weizmann Institute of Science.
- 1994 Teaching Assistant for the course, "Receptors and Recognition." Feinberg Graduate School, Weizmann Institute of Science.
- 1992 Teaching Assistant in mathematics for the course, "Introduction to Differential and Integral Calculus." Tel Aviv University.

• Membership on scientific advisory boards, and consulting activities

- Member of the Program Committee, RECOMB Regulatory Genomics 2006, (San Diego CA, USA).
- Member of the Program Committee, RECOMB 2005, (San Diego CA, USA)
- Member of the Program Committee, RECOMB Regulatory Genomics and Systems Biology 2005, (San Diego CA, USA).
- Member of the Program Committee, RECOMB Regulatory Genomics 2004, (San Diego CA, USA).
- 2001 - 2002 Consultant on modeling and structure prediction of G-protein coupled receptors. Pfizer, Inc., Cambridge, MA, USA.

• Membership on editorial boards

- Associate Editor, PLoS Computational Biology
- Associate Editor, Biology Direct

F: International Recognition

• Prizes, awards, and competitive scholarships

- 2007 Levinson Prize in Biology, awarded by the Scientific Council, Weizmann Institute of Science.
- 2006 James Heineman Research Award, (awarded by Minerva Stiftung).
- 2005 EMBO Young Investigator Award, awarded by the European Molecular Biology Organization.
- 2003 Fellowship from the Center for Complexity Sciences – a merit-based fellowship for young Principal Investigators (awarded by the Horowitz Foundation).
- 2002 Fellow of the PhRMA Foundation, a Center for Excellence in Integration of Genomics and Informatics, Harvard University.
- 2000 Fulbright Postdoctoral Award, awarded by the United States - Israel Educational Foundation.
- 1999 Prize of Distinction for outstanding Ph.D. studies. Awarded by the Feinberg Graduate School, Weizmann Institute of Science.
- 1998 First Prize in the National Competition for Multidisciplinary Ph.D. Study. Awarded by the Faculty of Mathematics and Natural Sciences, Hebrew University of Jerusalem.
- 1997 Fellowship of Distinction for outstanding achievement in studies and research. Awarded by the Dean of the Feinberg Graduate School, Weizmann Institute of Science.

• Invited talks at international meetings

1. 2007 The German Bioinformatics Conference, Potsdam, Germany.
2. 2007 The 9th International Northern European Bioinformatics Conference, Umeå, Sweden.
3. 2007 "Comparative genomics of translation efficiency." Guest lecturer in the seminar series, Dept. of Biology, Columbia University, New York, NY, USA.
4. 2007 "Comparative genomics of translation efficiency." Guest lecturer in the seminar series, Dept. of Biological Engineering, MIT, Cambridge, MA, USA.
5. 2006 "Differential gene expression regulation and species divergence." International course on "Global interrogations of biological processes," ISREC, Lausanne, Switzerland.

6. 2006 "Differential gene expression regulation and species divergence." Systems Biology and Evolution Workshop, Imperial College, London, UK.
7. 2006 "Coping with genetic and non-genetic stress." Baure Center for Genomics Research, Harvard University, Cambridge, MA, USA.
8. 2006 "Systems biology view of expression regulation." The 6th EMBO Young Investigator Meeting, Vienna, Austria.
9. 2006 "Coping with genetic and non-genetic perturbations." Guest lecturer in the seminar series of the Rockefeller Center for Studies in Physics and Biology, New York, NY, USA.
10. 2005 "Responsive backup circuits." The Yeast Systems Biology Network, Gotenburg, Sweden.
11. 2005 "Coupled sense and anti-sense regulation." The 3rd Bertinoro Computational Biology Meeting, Bertinoro, Italy.
12. 2005 "Transcription control of genetic backup circuits." EMBO Practical Course on Functional Genomics, Milan, Italy.
13. 2004 "Revealing the architecture of genetic backup circuits through inspection of transcription regulatory networks." The First Annual RECOMB Meeting on Regulatory Genomics, University of California at San Diego, San Diego, CA, USA.
14. 2003 "Computational detection and analysis of regulatory SNPs." The 5th International Northern European Bioinformatics Conference, Helsinki, Finland.
15. 2003 "Promoter sequence and the thermodynamics of DNA-protein interactions." The 2nd Annual McGill Workshop on Computational Biology, Barbados.
16. 2001 "Computational identification of genetics regulatory networks." DIMACS Workshop on Integration of Diverse Biological Data, Rutgers University, Piscataway, NJ, USA.

• **Invited talks at national meetings**

1. 2008 "Coping with genetic and non-genetic stress." ILANIT, Eilat, Israel.
2. 2004 "Promoter analysis of gene duplications reveals the architecture of genetic backup circuits." The Annual Meeting of the Israel Society of Genetics, (Haifa, Israel).
3. 2003 "Computational dissections of genetics regulatory networks." The 6th Israeli Bioinformatics Conference, Haifa, Israel.

• **Refereed international conference talks**

1. 2007 "Comparative genomics of translation regulation in yeast," a "Highlight Track" talk. ISMB, (Vienna Austria).
2. 2005 "Genome-wide transcription regulatory circuits controlling cellular malignant transformation." (One of 50 talks selected for oral presentation from 500 submissions. Lecture delivered by my student, since I was unable to attend.) Best Poster Award. ISMB, (Detroit, USA).
3. 2005 "Transcriptional reprogramming in genetic backup circuits." (One of 50 talks selected for oral presentation from 500 submissions. Lecture delivered by my student, since I was unable to attend.) ISMB, (Detroit, USA).
4. 2005 "Characterization of the effects of TF binding site variations on gene expression: Towards predicting the functional outcomes of regulatory SNPs." (Lecture delivered by my student.) RECOMB Regulatory Genomics and Systems Biology, (San Diego, USA).
5. 2005 "Backup by paralogs decouples genes lethality from centrality: evidence for preferential backup of hubs." RECOMB Regulatory Genomics and Systems Biology, (San Diego, USA).
6. 2005 "Phenotypic divergence correlates with translational control signals in protein coding sequences in yeast species." (Lecture delivered by my student.) RECOMB Regulatory Genomics and Systems Biology (San Diego, USA).

G: Scientific Productivity

• Competitive national and international grants (latest grant first)

- 2008 - 2012 "Expression regulatory networks: Beyond promoters and transcription control." European Research Foundation (ERC) "Ideas Grant," a personal competitive grant awarded by the EU. €1,300,000.
- 2004-present A non-competitive grant from the Ben May Foundation. \$105,000.
- 2007 - 2009 "Systems biology of regulatory networks." Minerva Foundation. €150,000.
- 2007 - 2008 "A potential role for non-coding RNA in regulating gene expression noise: a mathematical approach" (with T. Tlusty). Clore Center for Biological Physics, Weizmann Institute of Science. \$20,000.
- 2006 - 2010 "Evolutionary Conditioning," a non-competitive grant from the Tauber Foundation (with N. Eshel Ben-Jacob, et al.). \$200,000.
- 2006 - 2010 James Heineman Research Award, (awarded Minerva Stiftung) €60,000.
- 2006 - 2009 EMBO Young Investigator Award. European Molecular Biology Organization. €45,000.

- 2005 - 2010 "The effect of mutations on transcription regulation." European Union Network of Excellence in Bioinformatics. €300,000.
 - 2005 Grant from the Center for Systems Biology, Weizmann Institute of Science. \$10,000.
 - 2004 - 2007 "Deciphering the structure and logic of genetic regulatory networks and signaling pathways in multi-cellular organisms." Israel Science Foundation. \$240,000.
 - 2004 - 2006 "Computational dissections of transcription factor-promoter interactions." Minerva Foundation. €75,000
 - 2003 - 2004 Personal grant from the Horowitz Foundation Center for Complexity Sciences. \$88,000.
- **Students, Postdoctoral and Research Fellows**
- Dr. Itay Furman, 2006 - present. Programmer.
 - Dr. Orna Dahan, 2005 - present. Research Fellow.

Postdoctoral Fellows

- Dr. Naomi Siew, 2006 - present. Postdoctoral Fellow (shared with Prof. Dan Tawfik).
- Dr. Maria Rodríguez Martínez, 2006 - present. Postdoctoral Fellow (shared with Dr. Tsvi Ilusty).

Ph.D. Students

- Ran Kafri, 2003 - 2006. Ph.D. student. (Graduated with Distinction on the Dean's List). Currently a postdoctoral fellow with Prof. Marc Kirschner, Harvard Medical School.
- Michal Lapidot, 2003 - present. Ph.D. student. (Recipient of the Horowitz Foundation Center for Complexity Sciences Award).
- Amir Mitchell, 2004 - present. Ph.D. student.
- Reut Shalgi, 2005 - present. Ph.D. student (shared with Moshe Oren). (Recipient of the Horowitz Foundation Center for Complexity Sciences Award. Recipient of the Lee Segal Award of Mathematical Biology Lee Segal Award for Mathematical Applications to Biological Systems).
- Orna Man, 2005 - 2007. Ph.D. student. (Graduated with distinction; Recipient of the Daniel Brenner Memorial Prize, awarded by the Feinberg Graduate School, Weizmann Institute of Science).
- Ilya Venger, 2005 - present. Ph.D. student (shared with Dr. Asaph Aharoni).
- Ophir Shalem, 2007 - present. Ph.D. student
- Zohar Bloom, 2007 - present. Ph.D. student.

M.Sc. Students

- Reut Shalgi, 2003 - 2005. M.Sc. student (shared with Prof. Ron Shamir).
- Yael Garten, 2003 - 2005. M.Sc. student. Currently Ph.D. student, Stanford University.
- Arren-Bar Even, 2004 - 2006. M.Sc. student (shared with Prof. Naama Barkai). (Graduated with Distinction on the Dean's List). Currently working in industry.
- Ilana Lavie, 2004 - 2006. M.Sc. student (shared with Prof. Ronen Basri).
- Ophir Shalem, 2006 - 2007. M.Sc. student (shared with Dr. Eran Segal).
- Avihu Yona, 2007 - present. M.Sc. student.

• **National and international collaborators**

National:

- Dr. Asaph Aharoni, Dept. of Plant Sciences, Weizmann Institute of Science
- Prof. Naama Barkai, Dept. of Molecular Genetics, Weizmann Institute of Science
- Prof. Ronen Basri, Dept. of Computer Science and Applied Mathematics, Weizmann Institute of Science
- Prof. Eytan Domany, Dept. of Physics of Complex Systems, Weizmann Institute of Science
- Prof. Moshe Oren, Dept. of Immunology, Weizmann Institute of Science
- Prof. Varda Rotter, Dept. of Molecular Cell Biology, Weizmann Institute of Science
- Dr. Eran Segal, Dept. of Computer Science and Applied Mathematics, Weizmann Institute of Science
- Prof. Dan Tawfik, Dept. of Biological Chemistry, Weizmann Institute of Science

- Prof. Eshel Ben-Jacob, School of Physics and Astronomy, Tel-Aviv University
- Prof. David Horn, School of Physics and Astronomy, Tel-Aviv University
- Prof. Eytan Ruppin, MD, Ph.D., School of Computer Science and School of Medicine, Tel-Aviv University
- Prof. Ron Shamir, School of Computer Science, Tel-Aviv University

International:

- Prof. Duccio Cavalieri, Florence University
- Prof. Craig Hunter, Harvard University
- Prof. Roy Kishony, Harvard University
- Prof. Daniel Segre, Boston University

H: Patents

Provisionary patent application: "Global and local architecture of the mammalian microRNA-transcription factor regulatory network." In preparation by Yeda Research and Development Co., Ltd.

I. Languages

Hebrew: Reading: 3, Writing: 3, Speaking: 3

English: Reading: 3, Writing: 3, Speaking: 3

Scale: 1 (basic) to 3 (fluent)

List of Publications

Yitzhak Pilpel

Refereed Articles

29. Kafri R, Dahan O, Levy J & **Pilpel Y**. Preferential genetic backup of hubs in the protein interaction network: evidence for evolutionary selection for redundancy. *Proc Natl Acad Sci U S A* (2008, in press).
28. Lapidot M, Man-Mizrahi O, & **Pilpel Y**. Functional characterization of variations within regulatory motifs. *PLoS Genetics* (2008, in press).
27. Segal L,*Lapidot M,* Solan Z, Ruppin E, **Pilpel Y**, & Horn D. Nucleotide variation of regulatory motifs may lead to distinct expression patterns. *Bioinformatics* 2007 23(13):i440-9 (2007). ***These authors contributed equally to the work.**
26. Shalgi R, Leiber D, Oren M. & **Pilpel Y**. Global and local architecture of the mammalian microRNA-transcription factor regulatory network. *PLoS. Comput. Biol.* 3(7): e131 (2007).
25. Man O & **Pilpel Y**. Phenotypic divergence of yeast species is associated with differential translational efficiency of entire genetic modules. *Nature Genetics* 39(3): 415-421 (2007).
24. Lapidot M & **Pilpel Y**. Genome wide overview of natural antisense transcription --- how is it regulated, how does it regulate. *EMBO report* 7(12): 1216-1222 (2006).
23. Kafri R, Levi M & **Pilpel Y**. The regulatory utilization of genetic redundancy through responsive backup circuits. *Proc Natl Acad Sci U S A* 103(31): 11653-11658 (2006).
22. Xi Y, Shalgi R, Fodstad O, **Pilpel Y**, & Jingfang Ju. Differentially regulated miRNAs and actively translated mRNA transcripts by tumor suppressor p53 in colon cancer. *Clinical Cancer Research* 12(1): 2014-2024 (2006).
21. Bar-Even, A, Paulsson J, Maheshri N, Carmi M, O'Shea E, **Pilpel Y*** & Barkai N.* Noise in protein expression scales with natural protein abundance. *Nature Genetics* 36(6): 36-43 (2006). ***Corresponding authors.**
20. Nadejda S, Vardy E, Molshanski-Mor S, Eitan A, **Pilpel Y**, Schuldiner S, & Bibi E. 3D model of the *Escherichia coli* multidrug transporter MdfA reveals an essential membrane-embedded positive charge. *Biochemistry* 44(45): 14870-14880 (2005).
19. Shalgi R, Lapidot M, Shamir R & **Pilpel Y**. A catalog of stability-associated sequence elements in 3' UTRs of yeast mRNAs. *Genome Biology* 6(10): R86. (2005).
18. Tabach Y, Milyavsky M, Zuk O, Yitzhaki A, Shats I, Domany, E, Rotter, V & **Pilpel Y**. The promoters of human cell cycle genes integrate signals from two tumor suppressive pathways during cellular transformation. *Molecular Systems Biology* 1: 2005.002 (2005).

17. Kafri R, Bar-Even A. & **Pilpel Y**. Transcription control reprogramming in genetic backup circuits. *Nature Genetics* 37(3):295-299 (2005).
16. Garten Y,* Kaplan S* & **Pilpel Y**. Extraction of Transcription Regulatory Signals from Genome-wide DNA-protein interaction Data. *Nucleic Acids Research* 33(2): 605-615 (2005) ***These authors contributed equally to the work.**
15. Lapidot M & **Pilpel Y**. Comprehensive quantitative analyses of the effects of promoter sequence elements on mRNA transcription. *Nucleic Acid Research* 31: 3824-3828 (2003).
14. Sudarsanam P,* **Pilpel Y*** & Church GM. Genome-wide co-occurrence of promoter elements reveals a *cis*-regulatory cassette of rRNA transcription motifs in *S. cerevisiae*. *Genome Research* 12: 1723-1731 (2002). ***These authors contributed equally to the work.**
13. Zhu Z,* **Pilpel, Y*** & Church GM. Identification of transcription factor binding sites via a Transcription Factor-Centric Clustering (TFCC) algorithm. *J.Mol.Biol.* 318: 71-81 (2002). ***These authors contributed equally to the work.**
12. Cohen B, **Pilpel Y**, Mitra R & Church GM. Discrimination between the Yap1p and Yap2p transcriptional networks in yeast. *Mol. Biol. Cell.* 13: 1608-1614 (2002).
11. **Pilpel Y**, Sudarsanam P & Church GM. Identifying regulatory networks by combinatorial analysis of promoter elements. *Nature Genetics* 29: 153-159 (2001).
10. Fuchs T, Glusman G, Horn-Saban S, Lancet D. & **Pilpel Y**. The human olfactory subgenome: from sequence to structure and evolution. *Hum Genet* 108: 1-13 (2001).
9. Lapidot M, **Pilpel Y**, Gilad Y, Falcovitz A, Sharon D, Haaf T. & Lancet D. Mouse-Human Orthology Relationships in an Olfactory Receptor Gene Cluster. *Genomics* 71: 296-306 (2001).
8. Conticello SG, **Pilpel Y**, Glusman G & Fainzilber M. Position-specific codon conservation in hypervariable gene families. *Trends Genet* 16: 57-59 (2000).
7. Glusman G, Bahar A, Sharon D, **Pilpel Y**, White J & Lancet D. The olfactory receptor gene superfamily: data mining, classification, and nomenclature. *Mamm Genome* 11: 1016-1023 (2000).
6. **Pilpel Y**, Ben-Tal N & Lancet D. kPROT: a knowledge-based scale for the propensity of residue orientation in transmembrane segments. Application to membrane protein structure prediction. *J Mol Biol* 294: 921-935 (1999).

5. Sharon D, Glusman G, **Pilpel Y**, Khen M, Gruetzner F, Haaf T, & Lancet D. Primate evolution of an olfactory receptor cluster: diversification by gene conversion and recent emergence of pseudogenes. *Genomics* 61: 24-36 (1999).
4. **Pilpel Y** & Lancet D. The variable and conserved interfaces of modeled olfactory receptor proteins. *Protein Sci* 8: 969-977 (1999).
3. Segre D, Lancet D, Kedem O & **Pilpel Y**. Graded autocatalysis replication domain (GARD): kinetic analysis of self-replication in mutually catalytic sets. *Orig Life Evol Biosph* 28: 501-514 (1998).
2. Segre D, **Pilpel Y** & Lancet D. Mutual catalysis in sets of prebiotic organic molecules: Evolution through computer simulated chemical kinetics. *PhysicaA* 249: 558-564 (1998).
1. Lancet D, Kedem O & **Pilpel Y**. Emergence of order in small autocatalytic sets maintained far from equilibrium: application of a probabilistic receptor affinity distribution (RAD) model. *Ber Bunsenges Phys Chem* 98: 1166-1169 (1994).

Invited Editorials (News & Views)

2. Furman I. & **Pilpel Y**. Promoting mining of human promoters. News & Views in *Molecular Systems Biology* 2: 2006.0030 (2006).
1. Pilpel Y & Lancet D. Olfaction. Good reception in fruitfly antennae. News & Views in *Nature* 398: 285-287 (1999).

Book Chapters

1. Pilpel, Y, Sosinsky A & Lancet D. Molecular biology of olfactory receptors. *Essays Biochem* 33: 93-104 (1998).

Invited Reviews

1. Sharon D, Glusman G, **Pilpel Y**, Horn-Saban S. & Lancet D. Genome dynamics, evolution, and protein modeling in the olfactory receptor gene superfamily. *Ann NY Acad Sci* 855: 182-193 (1998).

Refereed Conference Proceedings

2. Lapidot M & **Pilpel Y**. Characterization of the Effects of TF Binding Site Variations on Gene Expression. Towards Predicting the Functional Outcomes of Regulatory SNPs. *Lecture Notes in Bioinformatics*, LNBI 4023 Proceedings, Springer-Verlag (2007).
1. Man O, Sussman JL & **Pilpel Y**. Examination of the tRNA Adaptation Index as a Predictor of Protein Expression Levels. *Lecture Notes in Bioinformatics*, LNBI 4023 Proceedings, Springer-Verlag (2007).